Skeletal Multiomic Atlas:

Quick Start Tutorial

and Case Studies

This tutorial provides step-by-step guidance on how to use the Skeletal Multiomic Atlas. It is intended as a quick-start guide for new users. It covers navigation from the homepage, use of the three main tools, and demonstration through three flagship case studies.

Quick Start: How to Use the Atlas

From the Homepage

The homepage of the Skeletal Multiomic Atlas presents three main entry **tools** (Figure 1):

1. **Human Reference Atlas** (Human healthy reference, multi-omic integration)
2. **Mouse Reference Atlas** (Mouse healthy reference, multi-omic integration)
3. **Experiment Expression Viewer** (individual studies, mouse and human, including disease datasets)

Besides the two "multiomics reference atlas" and the "expression viewer", users can find advanzed **tools** in upper tab. These tools are Co-expression, Coefficient variant calculator and Expression Comparator (cross-study exploratory comparisons)

Click on the icon or title of the tool you wish to use.

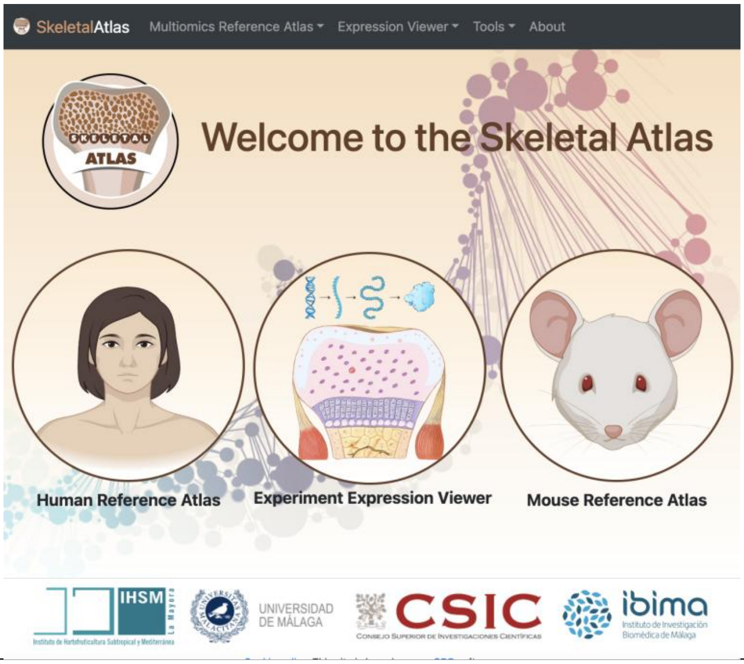


Figure 1. Front page of the Skeletal Atlas website, showing the three main entry points: Multiomics Reference Atlas, Experiment Expression Viewer, and Tools in upper tab.

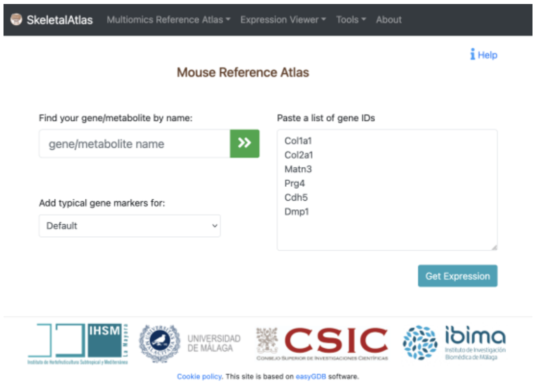
Tool 1 — Multiomics Reference Atlas

Mouse or Human Reference Atlas

When to use: To survey baseline expression across mouse or human skeletal tissues using single-cell RNA-seq, bulk RNA-seq, and proteomics.

Input screen (Figure 2): Type a gene symbol (e.g., Col1a1) or paste a list of genes. Default skeletal marker list is provided. Click 'Get Expression'.

Output screen (Figure 3): Interactive panels showing expression in scRNA-seq, bulk RNA-seq, and proteomics. Additional views: bar graphs, heatmaps, replicates plots, and average values tables.



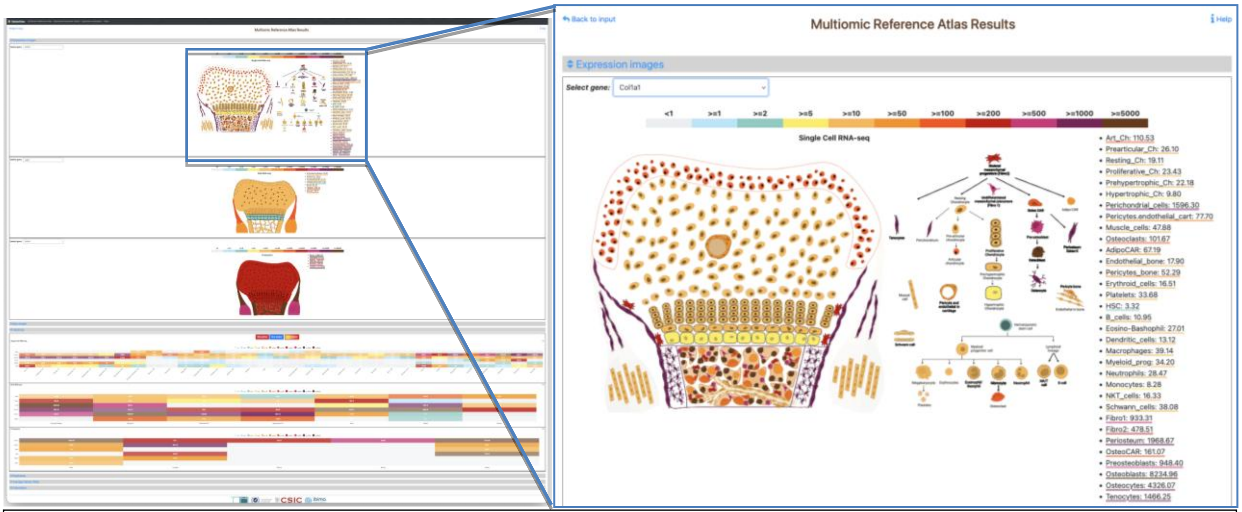
Find your gene/metabolite by name: gene/metabolite name

Add typical gene markers for: Default

Paste a list of gene IDs:
Col1a1
Col2a1
Matn3
Prg4
Cdh5
Dmp1

Cookie policy. This site is based on easyGDB software.

Figure 2. Input screen of the Multiomics Reference Atlas, where



Select gene: Col1a1

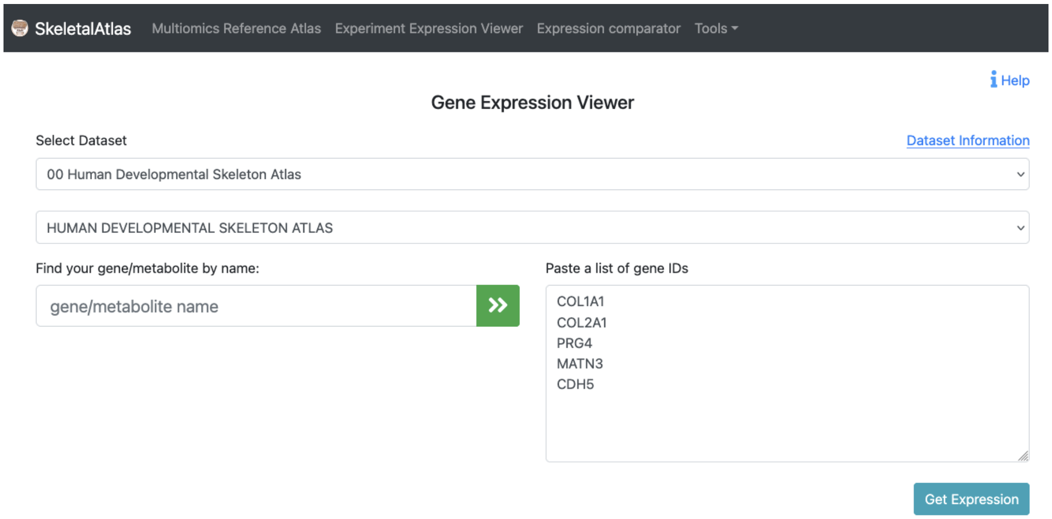
- Art_Ch: 110.53
- Prearticular_Ch: 26.10
- Resting_Ch: 19.11
- Proliferative_Ch: 23.43
- Prehypertrophic_Ch: 22.18
- Hypertrophic_Ch: 9.80
- Perichondrial_cells: 1596.30
- Pericytes.endothelial_cart: 77.70
- Muscle_cells: 47.88
- Osteoclasts: 101.67
- AdipoCAR: 67.19
- Endothelial_bone: 17.90
- Pericytes_bone: 52.29
- Erythroid_cells: 16.51
- Platelets: 33.68
- HSC: 3.32
- B_cells: 10.95
- Eosino-Bashophil: 27.01
- Dendritic_cells: 13.12
- Macrophages: 39.14
- Myeloid_prog: 34.20
- Neutrophils: 28.47
- Monocytes: 8.28
- NKT_cells: 16.33
- Schwann_cells: 38.08
- Fibro1: 933.31
- Fibro2: 478.51
- Periosteum: 1968.67
- OsteoCAR: 161.07
- Preosteoblasts: 948.40
- Osteoblasts: 8234.96
- Osteocytes: 4326.07
- Tenocytes: 1466.25

Figure 3. Multiomic Refference Atlas Output view: 3a. Detailed view of the Single Cell RNA-seq output, displaying cell populations and gene expression. 3b. Broad overview of the Multiomics Reference Atlas results page, showing multiple visualization panels including expression images, heatmaps, and replicates.

Tool 2 — Experiment Expression Viewer (Single Studies)

When to use: To explore expression data from a single published study (human or mouse, healthy or diseased).

Input screen (Figure 4): Select category (e.g., Human Developmental Atlas, Mouse bulk RNAseq, Human scRNAseq) and then select a dataset. Input genes and click 'Get Expression'.



Select Dataset: 00 Human Developmental Skeleton Atlas

HUMAN DEVELOPMENTAL SKELETON ATLAS

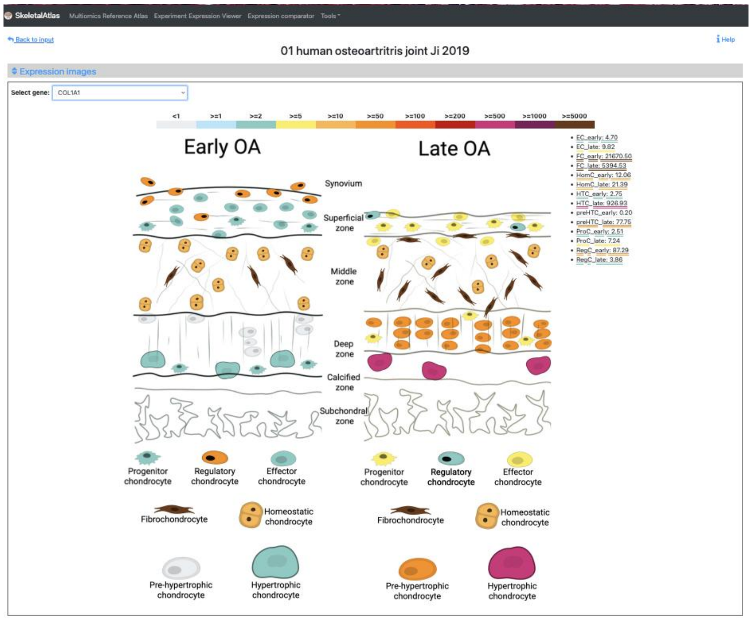
Find your gene/metabolite by name:

Paste a list of gene IDs:

COL1A1
COL2A1
PRG4
MATN3
CDH5

Figure 4. Input page of the Human Developmental Skeleton Atlas dataset, showing query options for gene expression analysis.

Output screen (figure 5): Study-specific interactive illustrations (where available), expression plots, heatmaps, replicates, and average values.



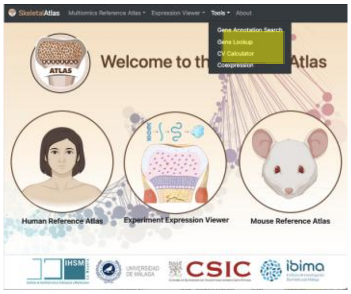
01 human osteoartritris joint Ji 2019

Select gene: COL1A1

- EC_early: 4.70
- EC_late: 9.82
- FC_early: 21670.50
- FC_late: 5394.53
- HomC_early: 12.06
- HomC_late: 21.39
- HTC_early: 2.75
- HTC_late: 926.93
- preHTC_early: 0.20
- preHTC_late: 77.75
- ProC_early: 2.51
- ProC_late: 7.24
- RegC_early: 87.29
- RegC_late: 3.86

Figure 5. Example of the Osteoarthritis study output (Experiment Expression Viewer), illustrating side-by-side comparison of Early OA and Late OA tissues with associated cell populations.

Advanced Tools:

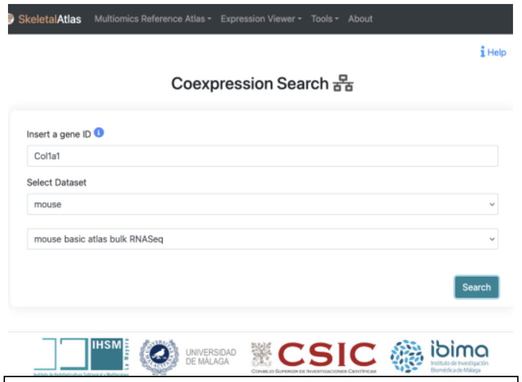


To support deeper analysis of datasets in the atlas, several tools are provided in the main tab: *Gene Annotation Search*, to search for generic information about individual genes of interest; Gene Lookup, to identify gene ID across databases or species; and three advanced tools: CV Calculator, Coexpression and Gene expression comparator, which will be explained next:

Co-expression:

When to use: Use this tool to quickly discover genes that show a similar expression pattern to a gene of interest within a specific study (bulk RNA-seq or single-cell), helping you identify putative co-regulated genes, pathways, or cell-type markers.

Input screen (Figure 6): Enter the gene symbol you want to analyze, choose the Organism (Mouse or Human), then open the Dataset tab to select the exact study (bulk or single-cell) where the gene's expression pattern will be analyzed to find similarly expressed genes by tissue or cell lineage.



Insert a gene ID: Col1a1

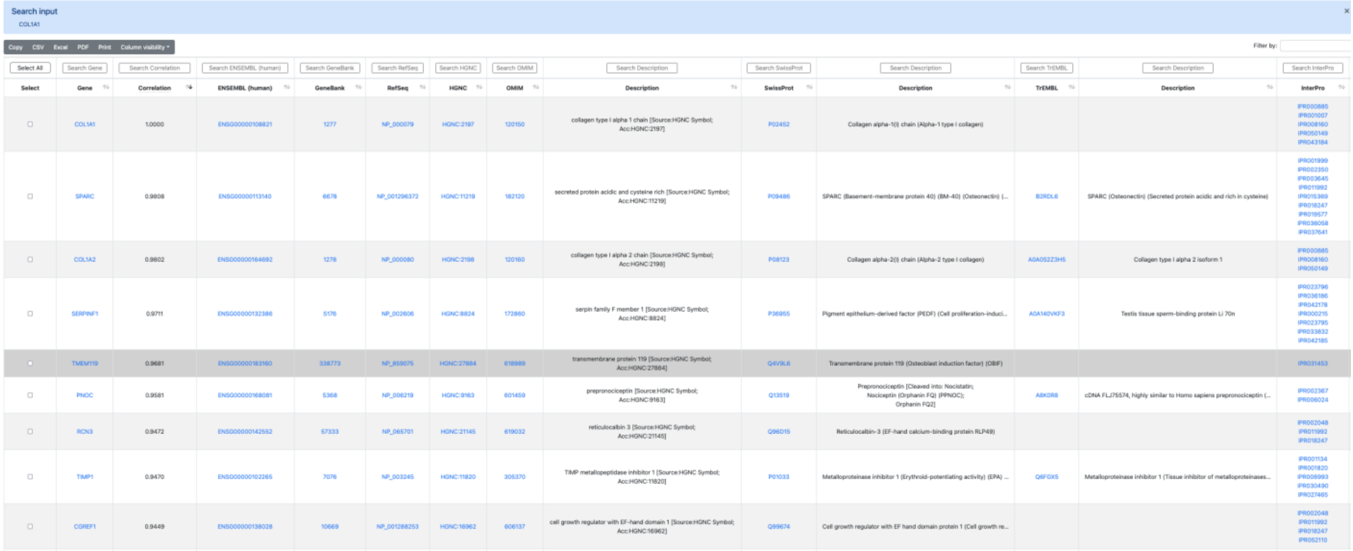
Select Dataset: mouse

mouse basic atlas bulk RNASeq

Figure 6. Input screen of the co-expression tool. Example of search for the gene Col1a1

Output screen (Figure 7): Results table beginning with your input gene, followed by genes with correlation ≥ 0.8, ordered from highest to lowest correlation. The table includes several downloading options: CSV, Excel, PDF.

Each gene includes links to referenced information (e.g., gene pages, publications).



Search input
COL1A1

Select	Gene	Correlation	ENSEMBL (human)	GeneBank	RefSeq	HGNC	OMIM	Description	SwissProt	Description	TrEMBL	Description	InterPro
☐	COL1A1	1.0000	ENSG00000108821	1277	NP_000079	HGNC:2197	120150	collagen type I alpha 1 chain [Source:HGNC Symbol; Acc:HGNC:2197]	P02452	Collagen alpha-1(I) chain (Alpha-1 type I collagen)			IPR000885 IPR001007 IPR008160 IPR050149 IPR043184
☐	SPARC	0.9808	ENSG00000113140	6678	NP_001296372	HGNC:11219	182120	secreted protein acidic and cysteine rich [Source:HGNC Symbol; Acc:HGNC:11219]	P09486	SPARC (Basement-membrane protein 40) (BM-40) (Osteonectin) (...	B2RDL6	SPARC (Osteonectin) (Secreted protein acidic and rich in cysteine)	IPR001999 IPR002350 IPR003645 IPR011992 IPR015369 IPR018247 IPR019577 IPR036058 IPR037641
☐	COL1A2	0.9802	ENSG00000164692	1278	NP_000080	HGNC:2198	120160	collagen type I alpha 2 chain [Source:HGNC Symbol; Acc:HGNC:2198]	P08123	Collagen alpha-2(I) chain (Alpha-2 type I collagen)	A0A0S2Z3H5	Collagen type I alpha 2 isoform 1	IPR000885 IPR008160 IPR050149
☐	SERPINF1	0.9711	ENSG00000132386	5176	NP_002606	HGNC:8824	172860	serpin family F member 1 [Source:HGNC Symbol; Acc:HGNC:8824]	P36955	Pigment epithelium-derived factor (PEDF) (Cell proliferation-induci...	A0A140VKF3	Testis tissue sperm-binding protein Li 70n	IPR023796 IPR036186 IPR042178 IPR000215 IPR023795 IPR033832 IPR042185
☐	TMEM119	0.9681	ENSG00000183160	338773	NP_859075	HGNC:27884	618989	transmembrane protein 119 [Source:HGNC Symbol; Acc:HGNC:27884]	Q4V9L6	Transmembrane protein 119 (Osteoblast induction factor) (OBIF)			IPR031453
☐	PNOC	0.9581	ENSG00000168081	5368	NP_006219	HGNC:9163	601459	prepronociceptin [Source:HGNC Symbol; Acc:HGNC:9163]	Q13519	Prepronociceptin [Cleaved into: Nocistatin; Nociceptin (Orphanin FQ) (PPNOC); Orphanin FQ2]	A8K0R8	cDNA FLJ75574, highly similar to Homo sapiens prepronociceptin (...	IPR002367 IPR006024
☐	RCN3	0.9472	ENSG00000142552	57333	NP_065701	HGNC:21145	619032	reticulocalbin 3 [Source:HGNC Symbol; Acc:HGNC:21145]	Q96D15	Reticulocalbin-3 (EF-hand calcium-binding protein RLP49)			IPR002048 IPR011992 IPR018247
☐	TIMP1	0.9470	ENSG00000102265	7076	NP_003245	HGNC:11820	305370	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol; Acc:HGNC:11820]	P01033	Metalloproteinase inhibitor 1 (Erythroid-potentiating activity) (EPA) ...	Q6FGX5	Metalloproteinase inhibitor 1 (Tissue inhibitor of metalloproteinases...	IPR001134 IPR001820 IPR008993 IPR030490 IPR027465
☐	CGREF1	0.9449	ENSG00000138028	10669	NP_001288253	HGNC:16962	606137	cell growth regulator with EF-hand domain 1 [Source:HGNC Symbol; Acc:HGNC:16962]	Q99674	Cell growth regulator with EF hand domain protein 1 (Cell growth re...			IPR002048 IPR011992 IPR018247 IPR052110

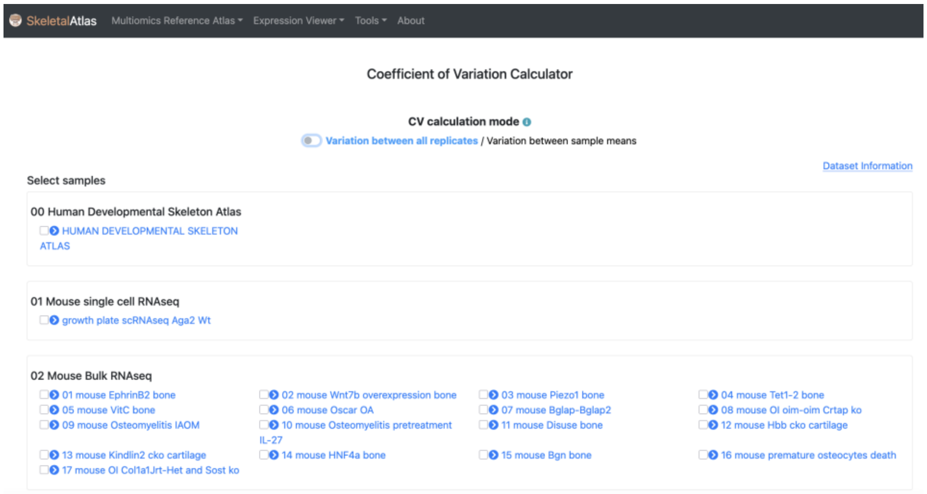
Figure 7. Output screen of the co-expression tool using an example in search of genes with similar expression pattern to Col1a1

Coefficient of Variation Calculator

When to use: Use this tool to evaluate the expression stability of genes across samples within one or several studies in the Skeletal Atlas. It helps identify genes with low variability (useful as reference or housekeeping genes) or assess the consistency of expression for genes of interest across biological replicates, tissues, or experimental conditions.

Input screen (Figure 8): In this screen, users can browse all available samples in the Skeletal Atlas, organized by study or publication. The user can then select whether to calculate the Coefficient of Variation using:

> Replicates — to assess technical or biological consistency within a study.
> or
> Mean of samples — to evaluate expression variability across averaged datasets.



Coefficient of Variation Calculator

CV calculation mode

○ Variation between all replicates / Variation between sample means

Dataset Information

Select samples

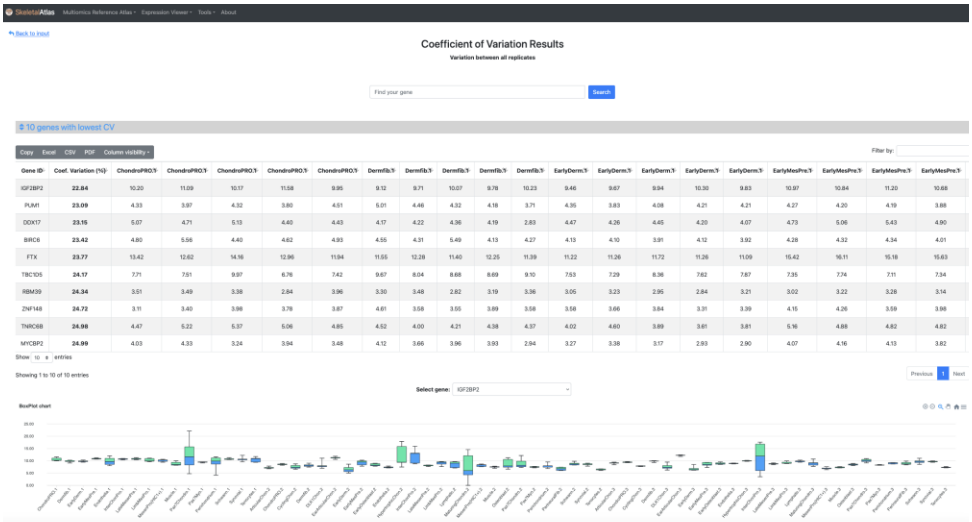
00 Human Developmental Skeleton Atlas
- ☐ HUMAN DEVELOPMENTAL SKELETON ATLAS

01 Mouse single cell RNAseq
- ☐ growth plate scRNAseq Aga2 Wt

02 Mouse Bulk RNAseq
- ☐ 01 mouse EphrinB2 bone
- ☐ 02 mouse Wnt7b overexpression bone
- ☐ 03 mouse Piezo1 bone
- ☐ 04 mouse Tet1-2 bone
- ☐ 05 mouse VitC bone
- ☐ 06 mouse Oscar OA
- ☐ 07 mouse Bglap-Bglap2
- ☐ 08 mouse OI oim-oim Crtap ko
- ☐ 09 mouse Osteomyelitis IAOM
- ☐ 10 mouse Osteomyelitis pretreatment IL-27
- ☐ 11 mouse Disuse bone
- ☐ 12 mouse Hbb cko cartilage
- ☐ 13 mouse Kindlin2 cko cartilage
- ☐ 14 mouse HNF4a bone
- ☐ 15 mouse Bgn bone
- ☐ 16 mouse premature osteocytes death
- ☐ 17 mouse OI Col1a1Jrt-Het and Sost ko

Figure 8. Input screen of the CV calculator. Users can select to perform analysis among any sample in the atlas

Output screen (Figure 9): Here users can find a summary table listing the 10 genes with the lowest CV, representing the most stably expressed genes in the selected dataset(s). Also, a search tab allows users to look up any gene of interest and instantly visualize its coefficient of variation across the chosen samples or studies. Below the table, a boxplot displays the expression distribution of the selected gene across all samples, providing a visual overview of its variation and stability.



Coefficient of Variation Results

Variation between all replicates

Gene ID	Coef. Variation (%)	ChondroPRO.	ChondroPRO.	ChondroPRO.	ChondroPRO.	ChondroPRO.	Dermfib.	Dermfib.	Dermfib.	Dermfib.	Dermfib.	EarlyDerm.	EarlyDerm.	EarlyDerm.	EarlyDerm.	EarlyDerm.	EarlyMesPre.	EarlyMesPre.	EarlyMesPre.	EarlyMesPre.
IGF2BP2	**22.84**	10.20	11.09	10.17	11.58	9.95	9.12	9.71	10.07	9.78	10.23	9.46	9.67	9.94	10.30	9.83	10.97	10.84	11.20	10.68
PUM1	**23.09**	4.33	3.97	4.32	3.80	4.51	5.01	4.46	4.32	4.18	3.71	4.35	3.83	4.08	4.21	4.21	4.27	4.20	4.19	3.88
DDX17	**23.15**	5.07	4.71	5.13	4.40	4.43	4.17	4.22	4.36	4.19	2.83	4.47	4.26	4.45	4.20	4.07	4.73	5.06	5.43	4.90
BIRC6	**23.42**	4.80	5.56	4.40	4.62	4.93	4.55	4.31	5.49	4.13	4.27	4.13	4.10	3.91	4.12	3.92	4.28	4.32	4.34	4.01
FTX	**23.77**	13.42	12.62	14.16	12.96	11.94	11.55	12.28	11.40	12.25	11.39	11.22	11.26	11.72	11.26	11.09	15.42	16.11	15.18	15.63
TBC1D5	**24.17**	7.71	7.51	9.97	6.76	7.42	9.67	8.04	8.68	8.69	9.10	7.53	7.29	8.36	7.62	7.87	7.35	7.74	7.11	7.34
RBM39	**24.34**	3.51	3.49	3.38	2.84	3.96	3.30	3.48	2.82	3.19	3.36	3.05	3.23	2.95	2.84	3.21	3.02	3.22	3.28	3.14
ZNF148	**24.72**	3.11	3.40	3.98	3.78	3.87	4.61	3.58	3.55	3.89	3.58	3.58	3.66	3.84	3.31	3.39	4.15	4.26	3.59	3.98
TNRC6B	**24.98**	4.47	5.22	5.37	5.06	4.85	4.52	4.00	4.21	4.38	4.37	4.02	4.60	3.89	3.61	3.81	5.16	4.88	4.82	4.82
MYCBP2	**24.99**	4.03	4.33	3.24	3.94	3.48	4.12	3.66	3.96	3.93	2.94	3.27	3.38	3.17	2.93	2.90	4.07	4.16	4.13	3.82

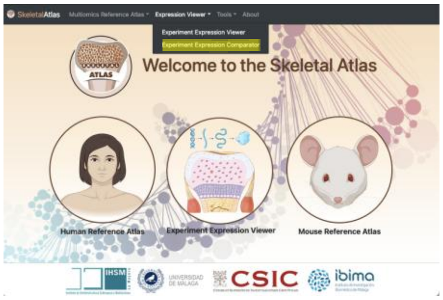
Show 10 entries

Showing 1 to 10 of 10 entries

Select gene: IGF2BP2

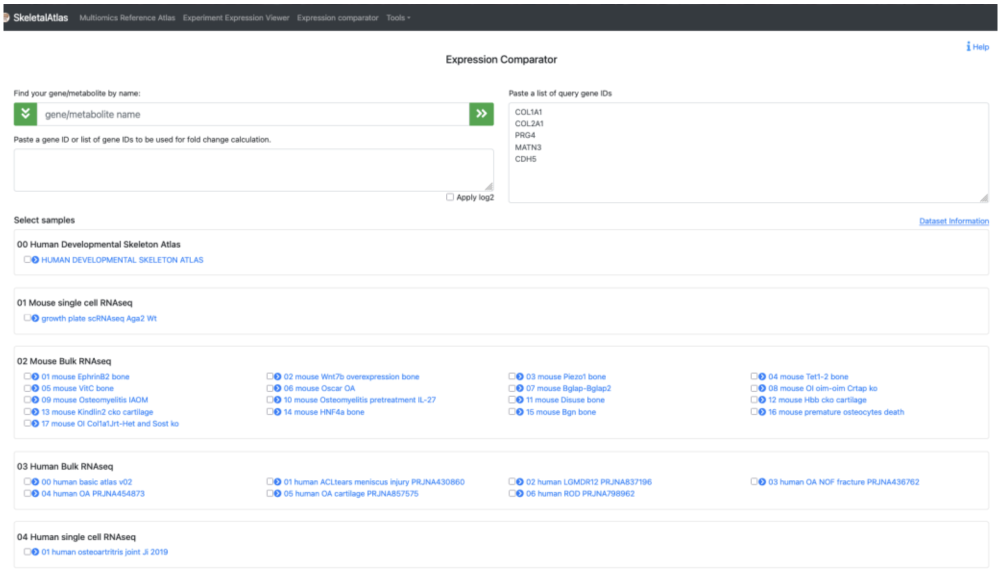
Figure 9. Output screen of the CV calculator tool using as an the single cell study of human development.

Expression Comparator (Exploratory, Cross-Study)



When to use: To compare gene expression across multiple datasets. Use with caution due to cross-study variability.

Input screen: Enter gene(s), optionally provide housekeeping genes for normalization, select log2 transformation, and select datasets (Figure 10) or individual samples/cell types (Figure 11).



Expression Comparator

Find your gene/metabolite by name:

gene/metabolite name

Paste a gene ID or list of gene IDs to be used for fold change calculation.

☐ Apply log2

Paste a list of query gene IDs

COL1A1
COL2A1
PRG4
MATN3
CDH5

Select samples

00 Human Developmental Skeleton Atlas

☐ HUMAN DEVELOPMENTAL SKELETON ATLAS

01 Mouse single cell RNAseq

☐ growth plate scRNAseq Aga2 Wt

02 Mouse Bulk RNAseq

☐ 01 mouse EphrinB2 bone
☐ 02 mouse Wnt7b overexpression bone
☐ 03 mouse Piezo1 bone
☐ 04 mouse Tet1-2 bone
☐ 05 mouse VitC bone
☐ 06 mouse Oscar OA
☐ 07 mouse Bglap-Bglap2
☐ 08 mouse OI oim-oim Crtap ko
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☐ 11 mouse Disuse bone
☐ 12 mouse Hbb cko cartilage
☐ 13 mouse Kindlin2 cko cartilage
☐ 14 mouse HNF4a bone
☐ 15 mouse Bgn bone
☐ 16 mouse premature osteocytes death
☐ 17 mouse OI Col1a1Jrt-Het and Sost ko

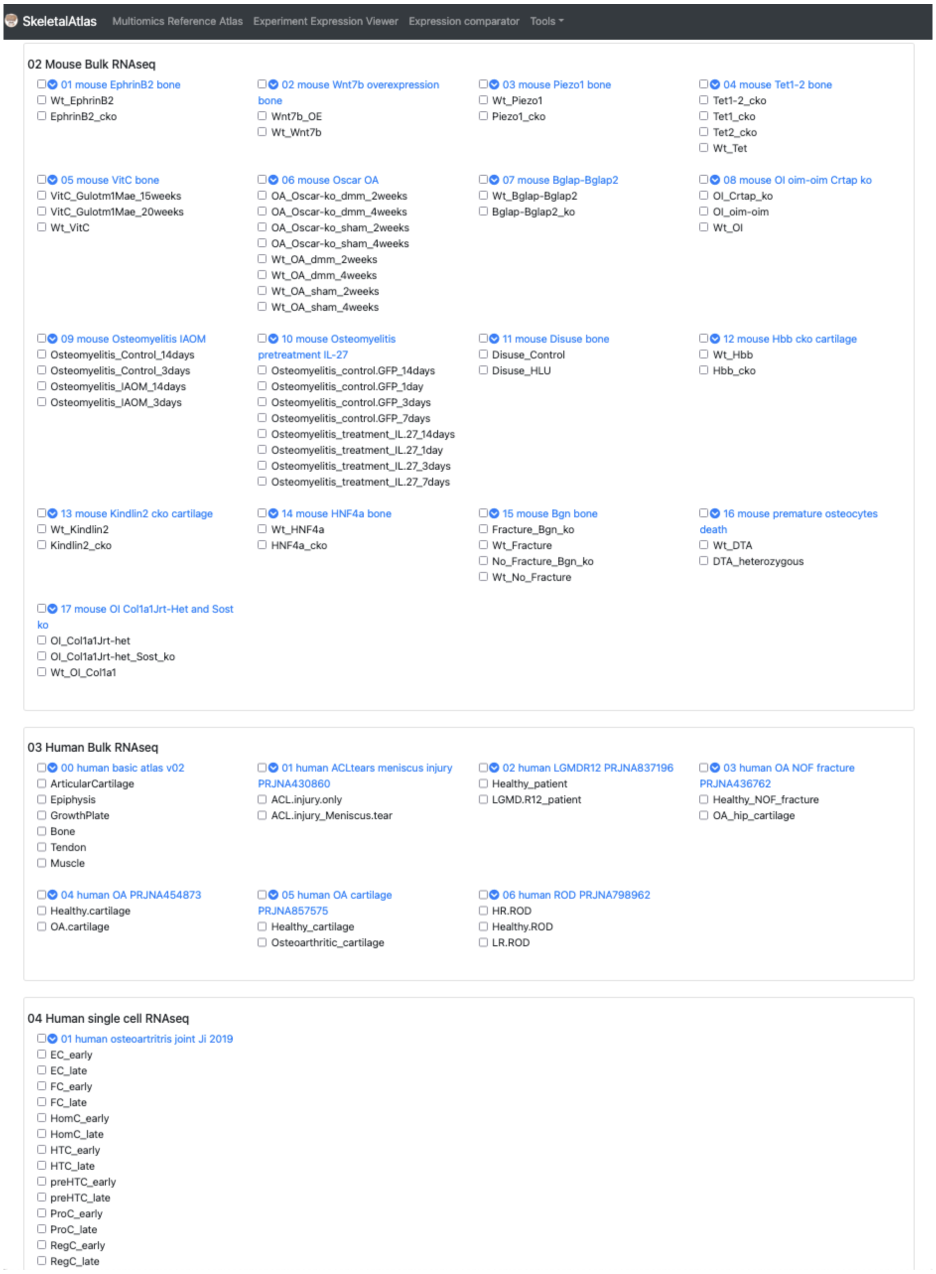
03 Human Bulk RNAseq

☐ 00 human basic atlas v02
☐ 01 human ACLtears meniscus injury PRJNA430860
☐ 02 human LGMDR12 PRJNA837196
☐ 03 human OA NOF fracture PRJNA436762
☐ 04 human OA PRJNA454873
☐ 05 human OA cartilage PRJNA857575
☐ 06 human ROD PRJNA798962

04 Human single cell RNAseq

☐ 01 human osteoartritris joint Ji 2019

Figure 10. Expression Comparator input page, where users can select multiple datasets and genes to perform cross-study comparisons.



02 Mouse Bulk RNAseq

☐ 01 mouse EphrinB2 bone
☐ Wt_EphrinB2
☐ EphrinB2_cko

☐ 02 mouse Wnt7b overexpression bone
☐ Wnt7b_OE
☐ Wt_Wnt7b

☐ 03 mouse Piezo1 bone
☐ Wt_Piezo1
☐ Piezo1_cko

☐ 04 mouse Tet1-2 bone
☐ Tet1-2_cko
☐ Tet1_cko
☐ Tet2_cko
☐ Wt_Tet

☐ 05 mouse VitC bone
☐ VitC_Gulotm1Mae_15weeks
☐ VitC_Gulotm1Mae_20weeks
☐ Wt_VitC

☐ 06 mouse Oscar OA
☐ OA_Oscar-ko_dmm_2weeks
☐ OA_Oscar-ko_dmm_4weeks
☐ OA_Oscar-ko_sham_2weeks
☐ OA_Oscar-ko_sham_4weeks
☐ Wt_OA_dmm_2weeks
☐ Wt_OA_dmm_4weeks
☐ Wt_OA_sham_2weeks
☐ Wt_OA_sham_4weeks

☐ 07 mouse Bglap-Bglap2
☐ Wt_Bglap-Bglap2
☐ Bglap-Bglap2_ko

☐ 08 mouse OI oim-oim Crtap ko
☐ OI_Crtap_ko
☐ OI_oim-oim
☐ Wt_OI

☐ 09 mouse Osteomyelitis IAOM
☐ Osteomyelitis_Control_14days
☐ Osteomyelitis_Control_3days
☐ Osteomyelitis_IAOM_14days
☐ Osteomyelitis_IAOM_3days

☐ 10 mouse Osteomyelitis pretreatment IL-27
☐ Osteomyelitis_control.GFP_14days
☐ Osteomyelitis_control.GFP_1day
☐ Osteomyelitis_control.GFP_3days
☐ Osteomyelitis_control.GFP_7days
☐ Osteomyelitis_treatment_IL.27_14days
☐ Osteomyelitis_treatment_IL.27_1day
☐ Osteomyelitis_treatment_IL.27_3days
☐ Osteomyelitis_treatment_IL.27_7days

☐ 11 mouse Disuse bone
☐ Disuse_Control
☐ Disuse_HLU

☐ 12 mouse Hbb cko cartilage
☐ Wt_Hbb
☐ Hbb_cko

☐ 13 mouse Kindlin2 cko cartilage
☐ Wt_Kindlin2
☐ Kindlin2_cko

☐ 14 mouse HNF4a bone
☐ Wt_HNF4a
☐ HNF4a_cko

☐ 15 mouse Bgn bone
☐ Fracture_Bgn_ko
☐ Wt_Fracture
☐ No_Fracture_Bgn_ko
☐ Wt_No_Fracture

☐ 16 mouse premature osteocytes death
☐ Wt_DTA
☐ DTA_heterozygous

☐ 17 mouse OI Col1a1Jrt-Het and Sost ko
☐ OI_Col1a1Jrt-het
☐ OI_Col1a1Jrt-het_Sost_ko
☐ Wt_OI_Col1a1

03 Human Bulk RNAseq

☐ 00 human basic atlas v02
☐ ArticularCartilage
☐ Epiphysis
☐ GrowthPlate
☐ Bone
☐ Tendon
☐ Muscle

☐ 01 human ACLtears meniscus injury PRJNA430860
☐ ACL.injury.only
☐ ACL.injury_Meniscus.tear

☐ 02 human LGMDR12 PRJNA837196
☐ Healthy_patient
☐ LGMD.R12_patient

☐ 03 human OA NOF fracture PRJNA436762
☐ Healthy_NOF_fracture
☐ OA_hip_cartilage

☐ 04 human OA PRJNA454873
☐ Healthy.cartilage
☐ OA.cartilage

☐ 05 human OA cartilage PRJNA857575
☐ Healthy_cartilage
☐ Osteoarthritic_cartilage

☐ 06 human ROD PRJNA798962
☐ HR.ROD
☐ Healthy.ROD
☐ LR.ROD

04 Human single cell RNAseq

☐ 01 human osteoartritris joint Ji 2019
☐ EC_early
☐ EC_late
☐ FC_early
☐ FC_late
☐ HomC_early
☐ HomC_late
☐ HTC_early
☐ HTC_late
☐ preHTC_early
☐ preHTC_late
☐ ProC_early
☐ ProC_late
☐ RegC_early
☐ RegC_late

Figure 11. Dataset selection screen within the Expression Comparator, displaying available mouse and human bulk and single-cell RNAseq datasets.

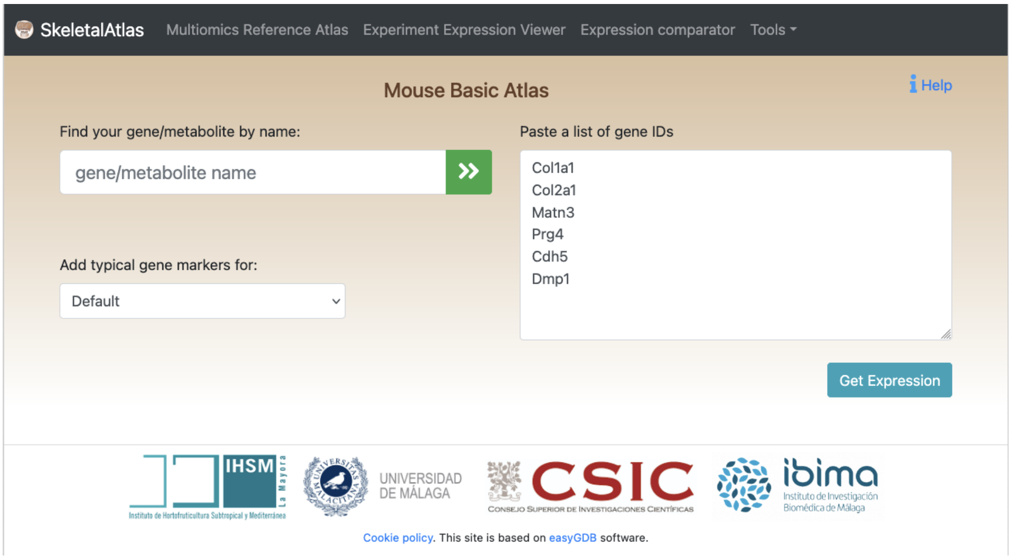
Output screen: Comparative plots and tables. Interpret as hypothesis-generating.

Best practice: Avoid cross-species comparisons; focus on within-species and comparable tissue/cell types.

Step-by-Step Example: Mouse Reference Atlas

This example illustrates a complete workflow in the Mouse Multiomics Reference Atlas, using the gene Col1a1 as a query. It shows input, output, and different visualization options.

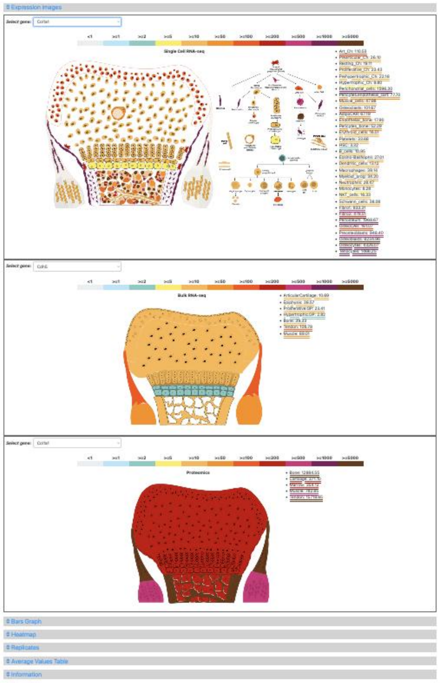
1. Input gene symbol (Figure 12): Enter at least Col1a1 in the query box and click 'Get Expression'.

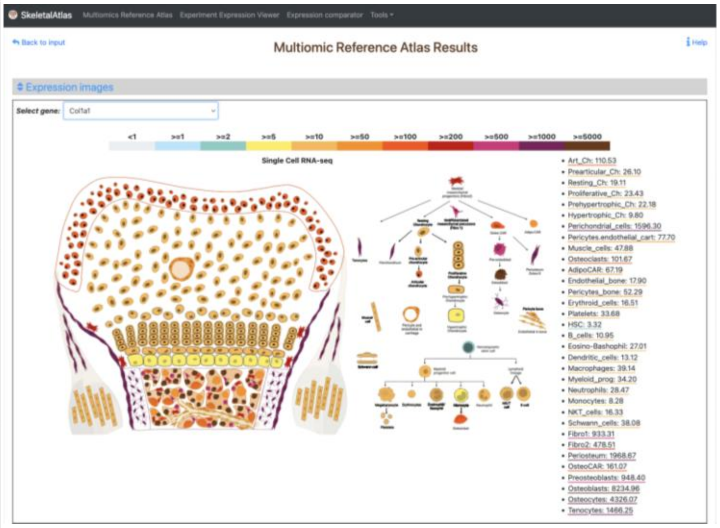


Col1a1
Col2a1
Matn3
Prg4
Cdh5
Dmp1

Figure 12. Input page for Mouse Basic Atlas, showing default skeletal marker genes provided for quick analysis.

2. <u>Expression output overview</u>: The output page shows three panels (Single-cell RNA-seq, Bulk RNA-seq, and Proteomics), each with tissue/cell-type annotations and color-coded expression intensities.





- Art_Ch: 110.53
- Prearticular_Ch: 26.10
- Resting_Ch: 19.11
- Proliferative_Ch: 23.43
- Prehypertrophic_Ch: 22.18
- Hypertrophic_Ch: 9.80
- Perichondrial_cells: 1596.30
- Pericytes.endothelial_cart: 77.70
- Muscle_cells: 47.88
- Osteoclasts: 101.67
- AdipoCAR: 67.19
- Endothelial_bone: 17.90
- Pericytes_bone: 52.29
- Erythroid_cells: 16.51
- Platelets: 33.68
- HSC: 3.32
- B_cells: 10.95
- Eosino-Bashophil: 27.01
- Dendritic_cells: 13.12
- Macrophages: 39.14
- Myeloid_prog: 34.20
- Neutrophils: 28.47
- Monocytes: 8.28
- NKT_cells: 16.33
- Schwann_cells: 38.08
- Fibro1: 933.31
- Fibro2: 478.51
- Periosteum: 1968.67
- OsteoCAR: 161.07
- Preosteoblasts: 948.40
- Osteoblasts: 8234.96
- Osteocytes: 4326.07
- Tenocytes: 1466.25

Figure 13. Left: Broad overview of the Multiomics Reference Atlas output, showing scRNA-seq, bulk RNAseq, and proteomics panels for Col1a1.

Right: Output from the Multiomics Reference Atlas (mouse), showing detailed gene expression patterns across skeletal tissues in single-cell resolution.

3. Alternative visualizations: Switch to 'Bars Graph' (Figure 14a), 'Heatmap' view (Figure 15), among other options, to compare Col1a1 expression across multiple tissues.

Figure 14. Bar graph visualization of Col1a1 and related genes across skeletal tissues in scRNA-seq, bulk RNAseq, and

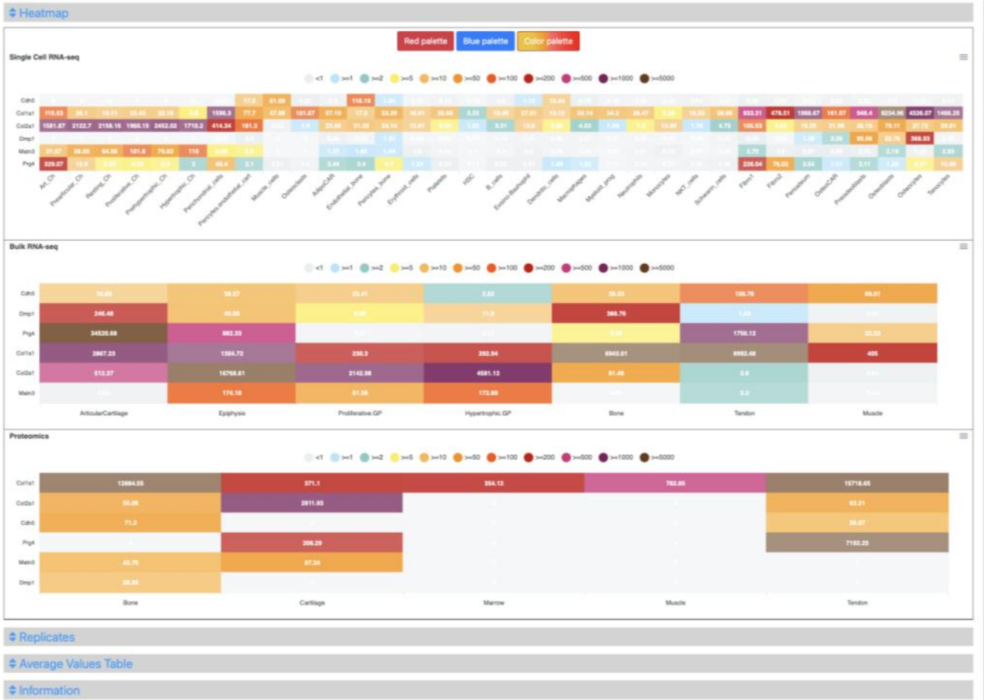


Figure 15. Heatmap visualization of Col1a1 and related genes across skeletal tissues in scRNA-seq, bulk RNAseq, and proteomics.

4. Replicates (Figure 16) and export options: Replicate plots show per-sample values, while the 'Average Values' table provides exportable CSV/Excel/PDF files.

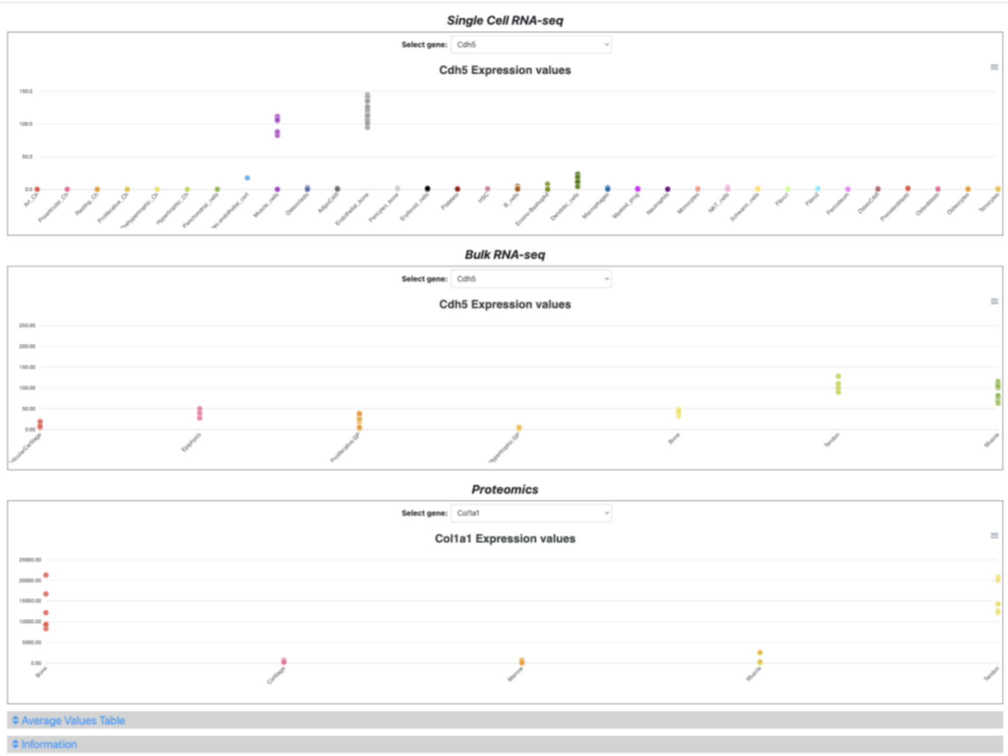


Figure 16. Replicates plots and average values table for Col1a1 expression across multiple tissues, with export options.

This step-by-step demonstration provides a template for users to follow when analyzing their own genes of interest.

Atlas Demonstration: Flagship Case Studies

Case Study 1: Human Developmental Skeleton Atlas (HCA collaboration)

Steps: Open Experiment Expression Viewer → 00 Human Developmental Skeleton Atlas. Query COL1A1, COL2A1, PRG4, MATN3. Explore interactive illustrations across 5.7–11.2 pcw.

Outputs: Stage-specific schematics of the knee joint, expression values, and cell hierarchies (Figure 17).

Take-home: A unique developmental single-cell/nucleus reference for human skeletal biology.

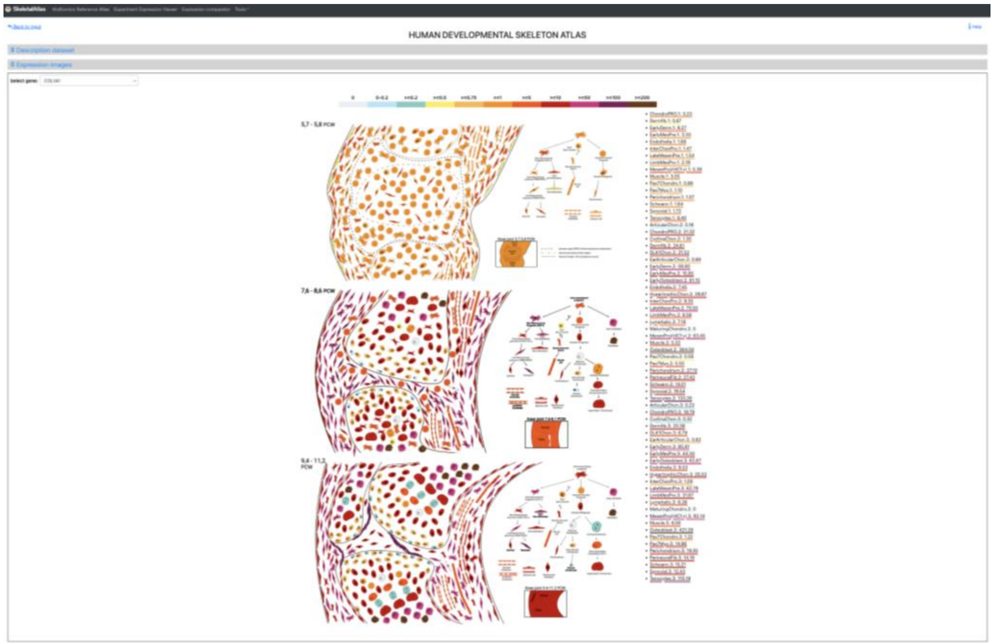


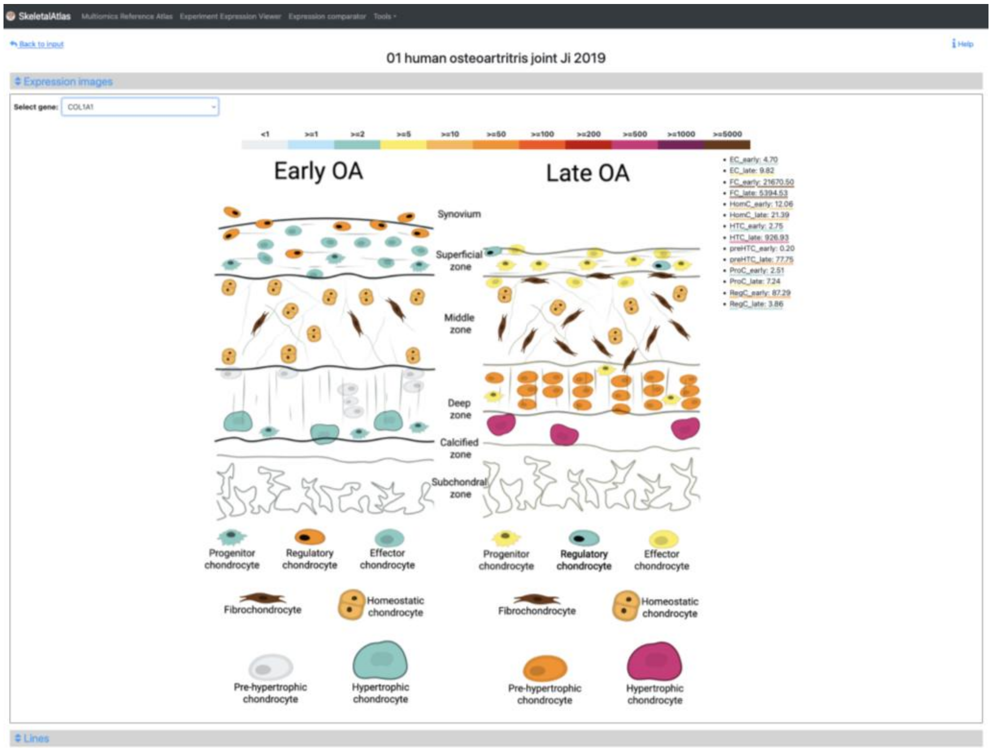
Figure 17. Human Developmental Skeleton Atlas (HCA): expression dynamics of COL2A1 across 5.7–11.2 pcw knee joint development.

Case Study 2: Human Osteoarthritis single-cell dataset

Steps: Experiment Expression Viewer → 04 Human scRNAseq → OA dataset (Ji 2019). Query COL1A1.

Outputs: Side-by-side illustrations of healthy/early OA vs. late OA cartilage, showing chondrocyte state shifts (Figure 18).

Take-home: Intuitive visualization of OA progression at single-cell resolution.



01 human osteoartritris joint Ji 2019

Select gene: COL1A1

- EC_early: 4.70
- EC_late: 9.82
- FC_early: 21670.50
- FC_late: 5394.53
- HomC_early: 12.06
- HomC_late: 21.39
- HTC_early: 2.75
- HTC_late: 926.93
- preHTC_early: 0.20
- preHTC_late: 77.75
- ProC_early: 2.51
- ProC_late: 7.24
- RegC_early: 87.29
- RegC_late: 3.86

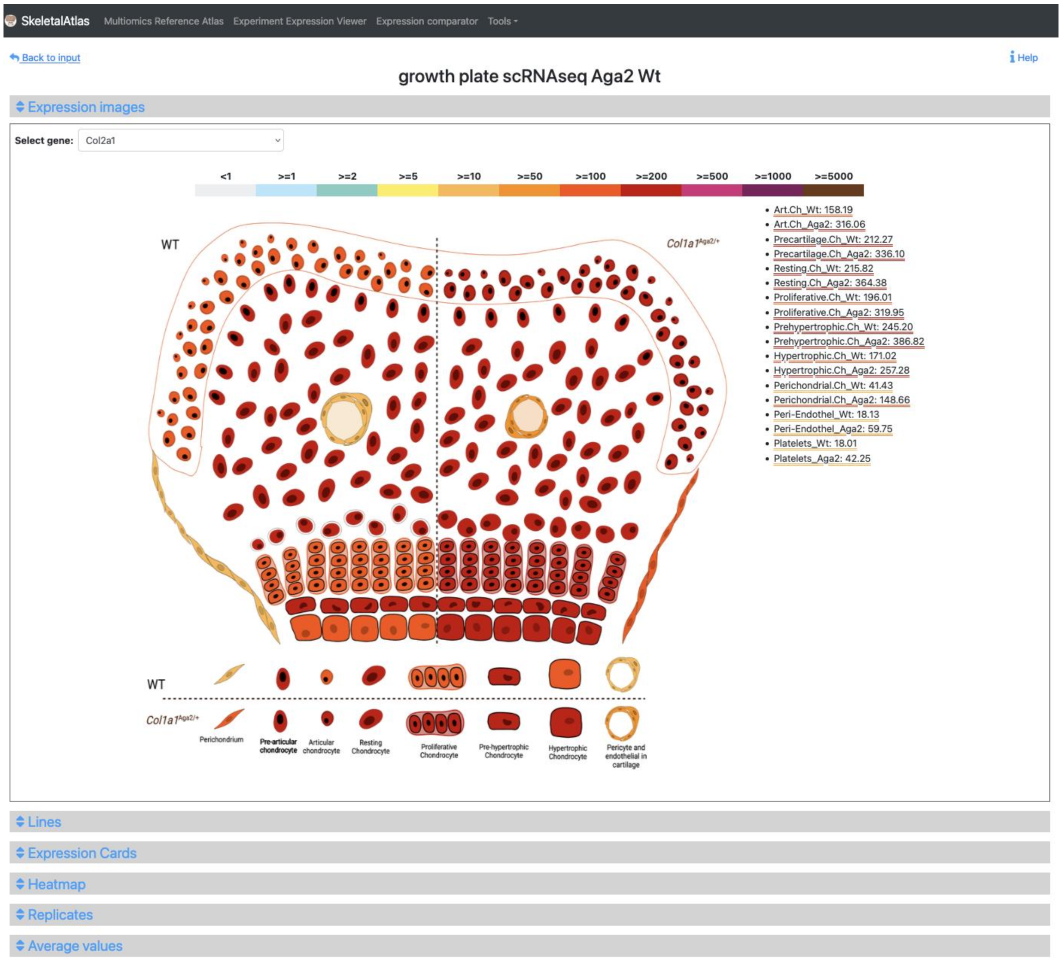
Figure 18. Human Osteoarthritis dataset: COL1A1 expression comparison between early OA and late OA cartilage, highlighting changes in chondrocyte populations.

Case Study 3: Mouse Osteogenesis Imperfecta single-cell model

Steps: Experiment Expression Viewer → 01 Mouse scRNAseq → Col1a1^{Aga2} (OI model). Query Col2a1 as key data in original study Zieba et al 2024.

Outputs: WT vs OI growth plate schematics with disrupted expression across chondrocyte maturation zones (Figure 19).

Take-home: Example of rare disease modeling in mouse, with potential for future expansion of the atlas.



- Art.Ch_Wt: 158.19
- Art.Ch_Aga2: 316.06
- Precartilage.Ch_Wt: 212.27
- Precartilage.Ch_Aga2: 336.10
- Resting.Ch_Wt: 215.82
- Resting.Ch_Aga2: 364.38
- Proliferative.Ch_Wt: 196.01
- Proliferative.Ch_Aga2: 319.95
- Prehypertrophic.Ch_Wt: 245.20
- Prehypertrophic.Ch_Aga2: 386.82
- Hypertrophic.Ch_Wt: 171.02
- Hypertrophic.Ch_Aga2: 257.28
- Perichondrial.Ch_Wt: 41.43
- Perichondrial.Ch_Aga2: 148.66
- Peri-Endothel_Wt: 18.13
- Peri-Endothel_Aga2: 59.75
- Platelets_Wt: 18.01
- Platelets_Aga2: 42.25

Figure 19. Mouse Osteogenesis Imperfecta model (Col1a1^{Aga2}): WT vs OI growth plate comparison showing disrupted chondrocyte zone expression.

Additional Datasets

The Atlas also includes:

- Mouse bulk RNAseq datasets (osteoporosis, osteomyelitis, genetic knockouts, etc.)
- Human bulk RNAseq datasets (OA, ACL injury, fracture, renal osteodystrophy, rare diseases)
- Proteomic datasets from skeletal tissues.

These can be explored individually or in comparison mode.

Export and Reproducibility

All result tables can be exported (Copy, CSV, Excel, PDF, Print). Users should document their dataset selection, housekeeping gene sets, and normalization choices when reporting results derived from the Atlas.